Cell motility: Turning failure into function

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CELL MOTILITY

Turning failure into function

In their search for more favorable environments, bacteria choose new directions to explore, usually at random. It is now shown in a marine bacterium with a single polar flagellum that this quest is enhanced by a buckling instability.

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When work began in the 1880s on the response of motile bacteria to gradients of chemical attractants, it was thought that cells swam directly toward a favorable source, hence the term 'chemotaxis'. The name has stuck, but we know now that cells use a stochastic strategy: they swim in a direction chosen more-or-less at random and then decide if life is getting better or worse. If life is getting better, their response is to continue along that course. In *E. coli*, a well-studied bacterium, cells 'run' along a smooth trajectory for a second or so, then 'tumble' for about 0.1 s, and then run in a new direction. The mean angle change between runs (~68°) is biased in the forward direction[1], and changes in angle are smaller when a cell is swimming up the gradient than when it is swimming down[2]. *E. coli* manages this because it has several flagellar filaments rotating in a bundle, pushing the cell forward. When one or more filaments change their direction of rotation from counter-clockwise to clockwise (viewed from behind the cell), the bundle comes apart and the cell tumbles. But what about bacteria that have only one flagellar filament projecting from a single pole? If they simply back up[3], space is not sampled very efficiently. Recently, it was found in a study of a polarly-flagellated marine bacterium *Vibrio alginolyticus*[4] that a cell swims forward, backs up, swims forward again, then suddenly flicks to the side by an angle with a broad distribution peaked at ~90°. This flicking strategy enables cells of *Vibrio* to accumulate near a point source of a chemical attractant much more efficiently than do cells of *E. coli*. A physical mechanism for how these cells

managed to flick was not firmly established, but one possibility suggested was a kink generated by an elastic instability[4]. Kwangmin Son and colleagues, as they describe in *Nature Physics*[5], now combine high-speed video with mechanical instability theory to show that the flick occurs when the proximal hook, under compression as the cell starts forward, undergoes a buckling instability. As they note, this is a benefit that accrues from controlled mechanical failure. Buckling does not occur later during forward swimming because steady swimming increases the hook's bending stiffness.

A bacterial flagellum has three parts, a basal body embedded in the cell wall, a helical filament extending out into the external medium, and a short proximal hook connecting the two. The basal body, with a diameter ~50 nm, is a reversible rotary motor powered by a proton flux (in *E. coli*) or a sodium-ion flux (in *V. alginolyticus*). Its stator comprises several force-generating units linked to the peptidoglycan layer (the rigid framework of the cell wall) that act upon the periphery of the rotor, a ring embedded in the inner (fluid) cell membrane. This ring is connected to the proximal hook by a drive shaft that passes through a bushing that spans the peptidoglycan layer and the outer cell membrane. The second part, the filament, has a diameter of ~20 nm and is a propeller designed for use at low Reynolds number. In *E. coli*, it is normally bent into a left-handed helix of diameter ~0.6 μm and pitch ~2.3 μm that is several micrometres long, but it can adopt several different polymorphic forms. The proximal hook, the third part of a bacterial flagellum, is a flexible coupling or universal joint with a diameter of ~20 nm. It is ~55 nm long in *E. coli* and ~100 nm long in *V. alginolyticus*.

The need for a flexible coupling was evident as soon as it was realized that bacterial flagella rotate[6]. *E. coli* and other peritrichously-flagellated organisms have motors located at random along the sides of the cell, whose filaments (when spinning counter-clockwise) coalesce into a bundle that pushes the cell steadily forward. The axis of the bundle is nearly parallel to the long axis of the cell (a rod ~1 μm in diameter by ~2 μm long), whereas the axes of the motors are nearly perpendicular to the long axis of the cell. So one needs a

flexible coupling, or universal joint, to get the torque around a 90° bend. Most of the angular compliance of the flagellum is in the hook[7,8], and cells with stiff hooks swim poorly[9]. The structure of most of the hook is known in atomic detail[10], and its length is specified by a molecular ruler[11]. When the hook of *Vibrio* buckles, the flagellar filament swings off axis and the cell body pivots, establishing a new direction of motion.

At first blush, one might think that a single polar flagellum is a more economical design than multiple peritrichous flagella, especially since flagellar bundles are not very efficient[12]. But most of the costs in this business are in the construction, not in the operation. Presumably, it's cheaper to place motors at random positions along the cell wall than it is to mount them on a specific platform at one pole. One benefit of the polar design might be enhanced swimming speeds; one cost a more constrained search paradigm. Nature appears to have stumbled upon a solution to the latter problem: a flick triggered by a buckling instability.

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1 Berg, H. C. & Brown, D. A. *Nature* **239**, 500–504 (1972).
2 Saragosti, J. *et al. Proc. Natl. Acad. Sci. USA* **108**, 16235–16240 (2011).
3 Taylor, B. L. & Koshland, D. E., Jr. *J. Bacteriol.* **119**, 640–642 (1974).
4 Xie, L., Altindal, T., Chattopadhyay, S. & Wu, X.-L. *Proc. Natl. Acad. Sci. USA* **108**, 2246–2251 (2011).
5 Son, K., Guasto, J. S. & Stocker, R. *Nature Phys* **9**, XXX–YYY (2013).
6 Berg, H. C. & Anderson, R. A. *Nature* **245**, 380–382 (1973).
7 Block, S. M., Blair, D. F. & Berg, H. C. *Nature* **338**, 514–517 (1989).
8 Block, S. M., Blair, D. F. & Berg, H. C. *Cytometry* **12**, 492–496 (1991).
9 Brown, M. T. *et al. J. Bacteriol.*, 3495–3501 (2012).
10 Samatey, F. A. *et al. Nature* **431**, 1062–1068 (2004).
11 Shibata, S. *et al. Molec. Microbiol.* **64**, 1404–1415 (2007).
12 Darnton, N. C., Turner, L., Rojevsky, S. & Berg, H. C. *J. Bacteriol.* **189**, 1756–1764 (2007).